Package ‘ifCNVR’

May 8, 2026

Title Isolation-Forest Based 'CNV' Detection from 'NGS' Data

Version 0.1.0

URL https://github.com/SimCab-CHU/ifCNVR

Description Automatically detects Copy Number Variations (CNV) from Next Generation Sequencing data using a machine learning algorithm, Isolation forest. More details about the method can be found in the paper by Cabello-Aguilar (2022) <doi:10.1101/2022.01.03.474771>.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

Imports data.table, rmarkdown, isotree

Depends R (>= 2.10)

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-02-15 19:40:02 UTC

Contents

`abSamples` *abSamples*

Description

abSamples

Usage

```
abSamples(readsMatrix, conta = "auto", q = 0.99, verbose = TRUE)
```

Arguments

`readsMatrix`	a matrix of the number of reads per target
`conta`	a parameter for the isotree function
`q`	quantile
`verbose`	a boolean

Value

the aberrant and normal samples

Examples

```
readsMatrix = data.frame(targets=paste0("target_",seq(1,50)), matrix(runif(500),nrow=50,ncol=10))
abSamples(readsMatrix)
```

`abTargets` *abTargets*

Description

abTargets

Usage

```
abTargets(readsMatrix, abSamples, opt = "regular", pred = 0.6)
```

Arguments

`readsMatrix`	the reads matrix
`abSamples`	the abSamples list result of the abSamples function
`opt`	"regular" or "extensive" a parameter
`pred`	a threshold on the isolation forest outlier prediction (range=[0,1[)

Value

a list of dataframes of the targets tagged as outliers

Examples

```
abTargets(readsMatrixExample,abSamples(readsMatrixExample))
```

`calculateRatio` *calculate Ratio*

Description

calculate Ratio

Usage

```
calculateRatio(readsMatrix, abSamples, roi, soi)
```

Arguments

`readsMatrix`	the reads matrix
`abSamples`	the abSamples list result of the abSamples function
`roi`	the region of interest
`soi`	the sample of interest

Value

the ratio associated with the abTargets

Examples

```
calculateRatio(readsMatrixExample, abSamples(readsMatrixExample), "EGFR-Ex20", "sample_2")
```

`calculateScore` *calculate Score*

Description

calculate Score

Usage

```
calculateScore(
  readsMatrix,
  abSamples,
  abTargets,
  roi = "Gene",
  sep = "-",
  thrScore = 7
)
```

Arguments

`readsMatrix`	a reads matrix with samples in columns and targets in lines (the first column are the targets)
`abSamples`	the abSamples list result of the abSamples function
`abTargets`	a list of dataframes of the targets tagged as outliers result of the abTargets() function
`roi`	the region of interest (Gene or Gene-Exon)
`sep`	a character the separator between roi in the bed file
`thrScore`	(default 0) a threshold on the localization score

Value

the score associated with the abSamples in the desired roi

Examples

```
abS <- abSamples(readsMatrixExample)
abT <- abTargets(readsMatrixExample,abSamples(readsMatrixExample))
calculateScore(readsMatrixExample, abS, abT, sep="-")
```

`CreateReadsMatrix` *CreateReadsMatrix*

Description

CreateReadsMatrix

Usage

```
CreateReadsMatrix(
  bamPath,
  bedFile,
  bedtoolsPath,
  outputFile = "n",
  verbose = TRUE
)
```

Arguments

`bamPath`	a path leading to the .bam and .bai files
`bedFile`	a path leading to the .bed file (Warning replace chrX by X in the position)
`bedtoolsPath`	the path leading to bedtools
`outputFile`	(optional) a path leading to a text file
`verbose`	a boolean

Value

a reads matrix

Examples

```
bamPath <- system.file("extdata/",package = "ifCNVR")
bed <- system.file("bedFile.bed",package = "ifCNVR")
bedtools <- 'n'
readsMatrix <- CreateReadsMatrix(bamPath, bed, bedtools)
```

`generateReport` *generateReport*

Description

generateReport

Usage

```
generateReport(outputFile = "n", readsMatrix, resTable, CNVpos)
```

Arguments

`outputFile`	a path to the html output file
`readsMatrix`	the reads matrix
`resTable`	the table result of the CalculateScore() function
`CNVpos`	the CNVpos list result of the abSamples function

Value

a html report

Examples

```
generateReport()
```

`normalizeReads` *normalizeReads*

Description

normalizeReads

Usage

```
normalizeReads(readsMatrix)
```

Arguments

`readsMatrix`	a reads matrix with samples in columns and targets in lines (the first column are the targets)

Value

a normalized reads matrix

Examples

```
normReads <- normalizeReads(readsMatrixExample)
```

`readsMatrixExample` *Example dataset*

Description

A dataset for the examples

Usage

```
readsMatrixExample
```

Format

A data frame with 11 rows and 6 variables:

targets the targets

sample_1 the number of reads in sample 1

sample_2 the number of reads in sample 2

sample_3 the number of reads in sample 3

sample_4 the number of reads in sample 4

sample_5 the number of reads in sample 5 ...

`scoring` *scoring*

Description

scoring

Usage

```
scoring(k, n, N)
```

Arguments

`k`	number of modified targets on the region
`n`	number of targets on the region
`N`	number of targets in the panel

Value

the confidence score

Examples

```
scoring(10,20,150)
```

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